FIGURE 5A

```
SGUS  ------MLYPINTETRGVFDLNGVWNFKLDYG----KGLEEKWYESKLTDT---ISMAVP   47
HGUS  LGLQGGMLYPQESPSRECKELDGLWSFRADFSDNRRRGFEEQWYRRPLWESGPTVDMPVP   60
EGUS  ------MLRPVETPTREIKKLDGLWAFSLDREN---CGIDQRWWESALQESR---AIAVP   48

SGUS  SSYNDIGVTKEIRNHIGYVWYEREFTVPAYLKD---QRIVLRFGSATHKAIVYVNGELVV  104
HGUS  SSFNDISQDWRLRHFVGWVWYEREVILPERWTQDLRTRVVLRIGSAHSYAIVWVNGVDTL  120
EGUS  GSFNDQFADADIRNYAGNVWYQREVFIPKGWAG---QRIVLRFDAVTHYGKVWVNNQEVM  105

GUS   EHKGGFLPFEAEINNSLRDG----MNRVTVAVDNILDDSTLPVG-LYSERHEEGLGKVIR  159
HGUS  EHEGGYLPFEADISNLVQVGPLPSRLRITIAINNTLTPTTLPPGTIQYLTDTSKYPKGYF  180
EGUS  EHQGGYTPFEADVTPYVIAG----KSVRITVCVNNELNWQTIPPG--MVITDENGKKK---  157

SGUS  -NKPNFDFFNYAGLHRPVKIYTTPFTYVEDISVVTDFNGPT--GTVTYTVDFQG-KAETV  215
HGUS  VQNTYFDFFNYAGLQRSVLLYTTPTTYIDDITVTTSVEQDS--GLVNYQISVKGSNLFKL  238
EGUS  -QSYFHDFFNYAGIHRSVMLYTTPNTWVDDITVVTHVAQDCNHASVDWQVVANG----DV  212

SGUS  KVSVVDEEGKVVASTEGLSGNVEIPNVILWEP-----LNTYLYQIKVELVNDGLT--ID  267
HGUS  EVRLLDAENKVVANGTGTQGQLKVPGVSLWWPYLMHERPAYLYSLEVQLTAQTSLGPVSD  298
EGUS  SVELRDADQQVVATGQGTSGTLQVVNPHLWQP-----GEGYLYELCVTAKSQTEC-----D  263

SGUS  VYEEPFGVRTVEVNDGKFLINNKPFYFKGFGKHEDTPINGRGFNEASNVMDFNILKWIGA  327
HGUS  FYTLPVGIRTVAVTKSQFLINGKPFYFHGVNKHEDADIRGKGFDWPLLVKDFNLLRWLGA  358
EGUS  IYPLRVGIRSVAVKGEQFLINHKPFYFTGFGFRHEDADLRGKGFDNVLMVHDHALMDWIGA  323

SGUS  NSFRTAHYPYSEELMRLADREGLVVIDETPAVGVHLNFMATTGLGEGSERVSTWEKIR--  385
HGUS  NAFRTSHYPYAEEVMQMCDRYGIVVIDECPGVGVGLAL------P-----QFFNNV  401
EGUS  NSYRTSHYPYAEEMLDWADEHGIVVIDETAAVGFNLSLGIGFEAGNKPKELYSEEAVNGE  383

SGUS  TFEHHQDVLRELVSRDKNHPSVVMWSIANEAATEEGAYEYFKPLVELTKELDPQKRPVT  445
HGUS  SLHHHMQVMEEVVRRDKNHPAVVMWSVANEPASHLESAGYYLKMVIAHTKSLDPS-RPVT  460
EGUS  TQQAHLQAIKELIARDKNHPSVVMWSIANEPDTRPQGAREYFAPLAEATRKLDPT-RPIT  442
```
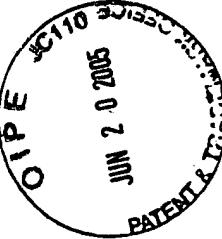
FIGURE 5B

```
SGUS  IVLFVMATPETDKVAELIDVIALNRYNGWYFDGGDLEAAKVHLRQEFHAWNKRCPGKPIM  505
HGUS  FVS--NSNYAADKGAPYVDVICLNSYYSWYHDYGHLELIQLATQFENWYKKYQ-KPII    517
EGUS  CVNVMFCDAHTDTISDLFDVLCLNRYYGWYVQSGDLETAEKVLEKELLAWQEKLH-QPII  501

SGUS  ITEYGADTVAGFHDIDPVMFTEEYQVEYYQANHVVFD--EFENFVGEQAWNFADFATSQG  563
HGUS  QSEYGAETIAGFHQDPPLMFTEEYQKSLLEQYHLGLDQKRRKYVVGELIWNFADFMTEQS  577
EGUS  ITEYGVDTLAGLHSMYTDMWSEEYQCAWLDMYHRVFD--RVSAVVGEQVWNFADFATSQG  559

SGUS  VMRVQGNKKGVFTRDRKPKLAAHVFRERWTNIPDFGYKN------  602
HGUS  PTRVLGNKKGIFTRQRQPKSAAFLLRERYWKIAN-ET--------  613
EGUS  ILRVGGNKKGIFTRDRKPKSAAFLLQKRWTGMNFGEKPQQGGKQ  603
```

FIGURE 5C

```
Staphyloccus : MVDLTSLYPINTETRGVFDLNGVWNFKLDYG-KGLEEKWYESKLTDTISMAVPSSY :  55
Staph homi   : ------------------------------------------------------- :   -
Staph warn   : ---LXLLHPITTGTRGGFALYGXXNLMLDYG-XGLTDTWTXSLLTELSRLVVLSWT :  52
Thermotoga   : -----MVRPQRNKKRFILILNGVWNLEVTSK------------D-RPIAVPGSW   :  36
Enb/Salmon   : ------------------------------------------------------- :   -
E coli       : ------MLRPVETPTREIKKLDGLWAFSLDRENCGIDQRWWESALQESRAIAVPGSF :  51

Staphyloccus : NDIGVTKEIRNHIGYVWYEREFTVPAYLKDQR--IVLRFGSATHKAIVYVNGELVV : 109
Staph homi   : ------------------------------------------------------- :   -
Staph warn   : THX-LTGEX-PAISILWPNSELTVSXLYXGSLXSSSXLCSSLTXHVVICQXVTLXV : 106
Thermotoga   : NEQ--YQDLCYEEGPFTYKTTFYVPKXLSQKH--IRLYFAAVNTDCEVFLNGEKVG :  88
Enb/Salmon   : ------------------------------------------------------- :   -
E coli       : NDQFADADIRNYAGNVWYQREVFIPKGWAGQR--IVLRFDAVTHYGKVWVNNQEVM : 105

Staphyloccus : EHKGGFLPFEAEIN-NSLRDGMNRVTVAVDNILDDSTLPVGLYSERHEEGLGKVIR : 164
Staph homi   : ------------------------------------------------------- :   -
Staph warn   : DHTGLIXXFEFMSTTCCXXDELVTGTLAX--ILYHXILPHGLYRKRHEXGLGKXNF : 160
Thermotoga   : ENHIEYLPFEVDVTGKVKSGENELRVVVEN-RLKVGGFPSKVPDSGTHTVGFFGSF : 143
Enb/Salmon   : ------------------------------------------------------- :   -
E coli       : EHQGGYTPFEADVTPYVIAGKSVRITVCVNNELNWQTIPPGMVITDENG----KKK : 157

Staphyloccus : NKPNFDFFNYAGLHRPVKIYTTPFTYVEDISVVTDFNGP---TGTVTYTVDFQGKA : 217
Staph homi   : ------------------------------------------------------- :   -
Staph warn   : YXLHFAFFXYAXLXRTVXMYX-NLVRXQDI-VVTX-HX-----XX-TVEQCVXXN- : 206
Thermotoga   : PPANFDFFPYGGIIRPVLIEFTDHARILDIWDTSESEPEKKLGKVKVKIEVSEEA  : 199
Enb/Salmon   : ------------GKLSPTPTAYIQDVTVXTDVLEN---TEQATVLGNVGADG     :  37
E coli       : QSYFHDFFNYAGIHRSVMLYTTPNTWVDDITVVTHVAQD---CNHASVDWQVVANG : 210
```

FIGURE 5D

```
Staphyloccus:  ET--VKVSVVDEEGKVVASTEGLSGNVEIPNVILWEPLNTYLYQIKVELVNDGLTI  :  271
Staph homi   :  -------------------GLSGNVEIPNVILWEPLNTYLYQIKVELVNDGLTI  :   35
Staph warn   :  KIXSVKITILDENDHAIXESEGAKGNVTIQNPILWQPLHAYLYNMKVELLNDNECV  :  262
Thermotoga   :  VGQEMTIKLGEEEKKIRTSNRFVEGEFILENARFWSLEDPYLYPLKVELEKD----  :  251
Enb/Salmon   :  D---IRVELRDGQQQIVAQGLGATGIFELDNPHLWEPGEGYLYELRVTCEAN-GEC  :   89
E coli       :  D---VSVELRDADQQVVATGQGTSGTLQVVNPHLWQPGEGYLYELCVTAKSQ-TEC  :  262

Staphyloccus:  DVYEEPFGVRTVEVNDGKFLINNKPFYFKGFGKHEDTPINGRGFNEASNVMDFNIL  :  327
Staph homi   :  DVYEEPFGVRTVEVNDGKFLINNKPFYFKGFGKHEDTPINGRGFNEASNVMDFNIL  :   91
Staph warn   :  DVYTERFGIRSVEVKDGQFLINDKPFYFKGFGKHEDTY-NGRGLNESANVMDINLM  :  317
Thermotoga   :  -EYTLDIGIRTISWDEKRLYLNGKPVFLKGFGKHEEFPVLGQGTFYPLMIKDFNLL  :  306
Enb/Salmon   :  DEYPVRVGIRSITXKGEQFLINHKPFYLTGFGFRHEDADFRGKGFDPVLMVHDHALM  :  145
E coli       :  DIYPLRVGIRSVAVKGEQFLINHKPFYFTGFGFRHEDADLRGKGFDNVLMVHDHALM  :  318

Staphyloccus:  KWIGANSFRTAHYPYSEELMRLADREGLVVIDETPAVGVH-LNFMATTGLGEGSER  :  382
Staph homi   :  KWIGANSFRTAHYPYSEELMRLADREGLVVIDETPAVGVH-LNFMATTGLGEGSER  :  146
Staph warn   :  KWIGANSFRTSHYPYSEEMRLADEQGIVVIDETXVGIH-LNFMXTLGGSX---A  :  369
Thermotoga   :  KWINANSFRTSHYPYSEEWLDLADRLGILVIDEAPHVGIT-------R---Y  :  348
Enb/Salmon   :  NWIGANSYRTSHYPYAEKMLDWADEHVIVINETAAGGFNTLSLGITFDAGERPKE  :  201
E coli       :  DWIGANSYRTSHYPYAEEMLDWADEHGIVVIDETAAVGFN-LSLGIGFEAGNKPKE  :  373

Staphyloccus:  VSTWEKIRTFE--HHQDVLRELVSRDKNHPSVVMWSIANEAATEEEGAYEYFKPL  :  435
Staph homi   :  VSTWEKIRTFE--HHQDVLRELVSRDKNHPSVVMWSIANEAATEEEGAYEYFKPL  :  199
Staph warn   :  HDTWXEFDTLE--FHKEVIXDLIXRDKNHAWVVMWXFGNEXGXNKGGAKAXFEPF  :  422
Thermotoga   :  HYNPETQKIAE------DNIRRMIDRHKNHPSVIMWSVANEPESNHPDAEGFFKAL  :  398
Enb/Salmon   :  LYSEEAINGETSQQAHLQAIKELIARDKNHPSVVCWSIANEPDTRPNGAREYFAPL  :  257
E coli       :  LYSEEAVNGET-QQAHLQAIKELIARDKNHPSVVMWSIANEPDTRPQGAREYFAPL  :  428
```

FIGURE 5E

```
Staphyloccus : VELTKELDPQKRPVTIVLFVMAT--PETDKVAELIDVIALNRYNGWYFDGGDLEAA : 489
Staph homi   : GGAAKELDPXKRPVTIVLFVMAT--PETDKVAELIDVIALNRYNGWYFDGGDLEAA : 253
Staph warn   : VNLAGEKDXXXXPVTIVTILXAX--RNVCEVXDLVDVVCLXXXXGWYXQSGDLEGA : 476
Thermotoga   : YETANEMDR-TRPVVMVSMMDAPDERTRDVALKYFDIVCVNRYYGWYIYQGRIEEG : 453
Enb/Salmon   : AKATRELDP-TRPITCVNVMFCD--AESDTITDLFDVVCLNRYYGWYVQSGDLEKA : 310
E coli       : AEATRKLDP-TRPITCVNVMFCD--AHTDTISDLFDVLCLNRYYGWYVQSGDLETA : 481


Staphyloccus : KVHLRQEFHAWNKRCPGKPIMITEYGADTVAGFHDIDPVMFTEEYQVEYYQANHVV : 545
Staph homi   : KVHLRQEFHAWNKRCPGKPIMITEYGADTVAGFHDIDPVMFTEEYQVEYYQANHVV : 309
Staph warn   : KXALDKEXXEWWKXQXNKPXMFTEYGVDXVVGLXXXPDKMXPEEYKMXFYKGYXKI : 532
Thermotoga   : LQALEKDIEELYARHR-KPIFVTEFGADAIAGIHYDPPQMFSEEYQAELVEKTIRL : 508
Enb/Salmon   : EQMLEQELLAWQSKLH-RPIIITEYGVDTLAGMPSVYPDMWSEKYQWKWLEMYHRV : 365
E coli       : EKVLEKELLAWQEKLH-QPIIITEYGVDTLAGLHSMYTDMWSEEYQCAWLDMYHRV : 536


Staphyloccus : FDEFENFVGEQAWNFADFATSQGVMRVQGNKKGVFTRDRKPKLAAHVFRERWTNIP : 601
Staph homi   : FDEFENFVGEQAWNFADFATSQGVMRVQGNKKGVFTRDRKPXLAAHVFRERRTNIP : 365
Staph warn   : MDK--------------------------------------------------- : 535
Thermotoga   : LLKKDYIIGTHVWAFADFKTPQNVRRPILNHKGVFTRDRQPKLVAHVLRRLWSEV- : 563
Enb/Salmon   : FDRGSVC------------------------------------------------ : 372
E coli       : FDRVSAVVGEQVWNFADFATSQGILRVGGNKKGIFTRDRKPKSAAFLLQKRWTGMN : 592


Staphyloccus : DFGYKN----- : 607
Staph homi   : DFGYKNASHHH : 376
Staph warn   : ----------- : -
Thermotoga   : ----------- : -
Enb/Salmon   : ----------- : -
E coli       : FGEKPQQGGKQ : 603
```

FIGURE 5F

```
B psm      : --------ATGGTAGATCTGACTAGT-CTGTACCGATCAACACCGAGACCCGTGGCGTCTTCGACCTCAATGGCGTCTG  :  71
Salmonella : CCNCCCNTTTNGTANCNTNTTTGNNANCTGCTGCANNNGATCACNACNNGANNCGGGNGGGTTCGNNCTCTATGGCNCGNG  :  84
Pseudomona : -------------------------------------------------------------------------------  :  -

B psm      : GAACTTCAAGCTGGACTACGGGAAAGGACTGGAAGAGAAGTGGTACGAAAGCAAGCTGACCGACACTATTAGTATGCCGTCCC  : 155
Salmonella : GAACNNNATGNTGGNCNACNGTTNANGACNTGAANAGTTGCTG-CCGA-ACTATCACTCAGNTCNTGNA  : 166
Pseudomona : -------TGCTGGACNACNGTTNAGGATTTTNAGACACNGNGGAGCTAAAGCTTGCTGACCN-AACTATCACGCGCNCGTGCA  :  75

B psm      : AAGCAGTTACAATGACATTGGCGTGACCAAGGAAATCCGCAACCATATCGGATATGT-CTGGTACGAACGTGAGTTCACGGT-G  : 237
Salmonella : AGTTGG--ACAAC-ACATTNCC-TGACANGNGAAAAGC-CCGCCATATCCATACTGTGCTGGCCCAACANTGAGTTCACNGTCG  : 245
Pseudomona : NGCTTGG-ACCGCGACATTNCC-TGACANGNGAAANACTCCGCCATATCCATCTT-TGCTGGCCCAACAGTGAGTTNACNGT-N  : 155

B psm      : CCGGCCTATCTGAAGGATCAGC-GTATCGTGCTCCGCTTCGGCCTTCAACTCACAAAGCAATT-GTCTATGTCAATG-GTGAG  : 318
Salmonella : TCGNACTNTATGANGGATCACCCGTGTATCGAACTCCGTTNATNTTCTNCAGCTAACATAACTGTGNGCATATGTCAATGNATGAC  : 329
Pseudomona : NCGNACNNTNNGANGGATCAGT-GNATCGAGCTCCNTTNANNTTCTNC-GCTAACATAACACATGTNGCATATGTCAATNAATNAC  : 237

B psm      : -CTGGTCG-TGGAGCACAAGGGCGG--ATTCCTGCCATTCGAAGCGGAAATCAACAACTC-GCTGCGTGATGGCATGAATCGCG  : 397
Salmonella : -CTGGTCGGTGNANCACACCGGGCGTNATTGGNGCGTNATTGNNATTCGAATTNATGTGNAATTCAACAACTTTGNTGCANGNTGGAATCTG  : 412
Pseudomona : GCTGGNCG-TGGANCNCACCGGGCTNATTGNGCGGCTNATTCGNNATTCGAATTNGNATGNCACAACTNTGNTGCACGNTGNGAANAATTGC  : 320

B psm      : TCACCGTCG-CCGTGGACAACATCCTCGACGATA-GCACCCTCCC--GGTGGGGCTGTACAGCGAGC-GCCACGAAGAGGGC-C  : 475
Salmonella : GGGCCAGGGACTTTGGCCANCTTCCTNAACCATTCGCANCCTCCCCCCAGTGGCTTGTACACNATTG-NGCCCCAAAAAGGC-N  : 494
Pseudomona : GTNACAGGGGACTTTGGCCN-CTTCCTAAACCATN-GCATCCTCCC---NATGGCGTGTACACGAATGNGCCCCAAAANGGCNT  : 399

B psm      : TCGGAAAAGTCATTCGTAACAAGCCGAAC-TTCGACTTCTTCAACTATGCAGGCCTCCGGTGAAAATC-TACACGAC  : 557
Salmonella : TCAGATAGG-CATTT-TGACAAGTCCAN-NTTAACTTTTTCAACTTTTTCAACTATGCNGNGNCCTGCACCGGAGACGCTGAAAAANGTACANGAN  : 575
Pseudomona : TCAGAAAGGCAATTNTNTAACAAGGCNGANNTTTGACTTTTTCAACTATGCAGNNCTGCACCGGACGCTGAAAATG-TACANGAC  : 482

B psm      : CCCGTTTACGTACGTCGAGGACATCTCGGTTGTGACCGACTTCAATGCCCAACCGGGACTGTGACCTATACGG--TGGACTTT  : 639
Salmonella : CCT-TGTACGTTCCACCAAGANATTAAGGTGTGACCCACNTCCATTTCCTAACNGGACTGTGACTNATAAAGGNTGACCNTI  : 658
Pseudomona : CCTGGGTACGTNCNACCAAGACATNNAAGTNGTGACCGACTCCATTGNCTAACCGGGACTGT-ACCTATAAATG--CGGACTAT  : 563

B psm      : CAAGGCAAAGCCGAGACCGTGAAAGTGTCGGTCGTGGATGAGGAAGGCAAAGTGGTCGCAAGCACCGAGCGGTAAC  : 723
Salmonella : CANGGACACACATTGCAA---TGACCCTTTNAAACGGACACACCAGGNTTAAAGG--AAAAACAAATTGGTTGGGNAGTCCAN  : 737
Pseudomona : CANGGCAATGCCGTNCNACGACACCAGGATNAGGAAANACAANTGGT--GGNANCNACCANGCCAGTGTCAC  : 643
```

FIGURE 5G

```
B psm      : GTGGAGATTCCGAATGTCATCCTCTGGGAACCACTGAACACGTATCTCTACCAGATCAAAGTGGAACTGGTGAACGACGGACTG : 807
Salmonella : CCAAGGGCCAATTANTTGTTNCNCGGGGANTAAANCCCCCN----------------------------------------- : 779
Pseudomona : G------------------------------------------------------------------------------------ : 644
```